



#3

TECH CENTER 1600/2900

JAN 15 2002

RECEIVED

1

SEQUENCE LISTING

<110> SHI-YOU
ADNEY, WILLIAM S.
VINZANT, TODD B.
HIMMEL, MICHAEL E.

<120> THERMAL TOLERANT EXOGLUCANASE FROM ACIDOTHERMUS
CELLULOLYTICUS

<130> 40197.4US01

<140> 09/917,376

<141> 2001-07-28

<160> 7

<170> PatentIn.Ver. 2.1

<210> 1

<211> 957

<212> PRT

<213> Acidothermus cellulolyticus

<220>

<221> MOD_RES

<222> (957)

<223> Any amino acid

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Gly Val Leu Pro Ile Ala Ile Thr Ala Ser Pro Ala His Ala Ala Thr
35 40 45

Thr Gln Pro Tyr Thr Trp Ser Asn Val Ala Ile Gly Gly Gly Gly Phe
50 55 60

Val Asp Gly Ile Val Phe Asn Glu Gly Ala Pro Gly Ile Leu Tyr Val
65 70 75 80

Arg Thr Asp Ile Gly Gly Met Tyr Arg Trp Asp Ala Ala Asn Gly Arg
85 90 95

Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly Tyr Asn
100 105 110

Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys Val Trp
115 120 125

Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp Gly Ala
130 135 140

→ #3 catalytic

Ile	Leu	Arg	Ser	Ser	Asp	Gln	Gly	Ala	Thr	Trp	Gln	Ile	Thr	Pro	Leu	145	150	155	160
Pro	Phe	Lys	Leu	Gly	Gly	Asn	Met	Pro	Gly	Arg	Gly	Met	Gly	Glu	Arg	165	170	175	
Leu	Ala	Val	Asp	Pro	Asn	Asn	Asp	Asn	Ile	Leu	Tyr	Phe	Gly	Ala	Pro	180	185	190	
Ser	Gly	Lys	Gly	Leu	Trp	Arg	Ser	Thr	Asp	Ser	Gly	Ala	Thr	Trp	Ser	195	200	205	
Gln	Met	Thr	Asn	Phe	Pro	Asp	Val	Gly	Thr	Tyr	Ile	Ala	Asn	Pro	Thr	210	215	220	
Asp	Thr	Thr	Gly	Tyr	Gln	Ser	Asp	Ile	Gln	Gly	Val	Val	Trp	Val	Ala	225	230	235	240
Phe	Asp	Lys	Ser	Ser	Ser	Ser	Leu	Gly	Gln	Ala	Ser	Lys	Thr	Ile	Phe	245	250	255	
Val	Gly	Val	Ala	Asp	Pro	Asn	Asn	Pro	Val	Phe	Trp	Ser	Arg	Asp	Gly	260	265	270	
Gly	Ala	Thr	Trp	Gln	Ala	Val	Pro	Gly	Ala	Pro	Thr	Gly	Phe	Ile	Pro	275	280	285	
His	Lys	Gly	Val	Phe	Asp	Pro	Val	Asn	His	Val	Leu	Tyr	Ile	Ala	Thr	290	295	300	
Ser	Asn	Thr	Gly	Gly	Pro	Tyr	Asp	Gly	Ser	Ser	Gly	Asp	Val	Trp	Lys	305	310	315	320
Phe	Ser	Val	Thr	Ser	Gly	Thr	Trp	Thr	Arg	Ile	Ser	Pro	Val	Pro	Ser	325	330	335	
Thr	Asp	Thr	Ala	Asn	Asp	Tyr	Phe	Gly	Tyr	Ser	Gly	Leu	Thr	Ile	Asp	340	345	350	
Arg	Gln	His	Pro	Asn	Thr	Ile	Met	Val	Ala	Thr	Gln	Ile	Ser	Trp	Trp	355	360	365	
Pro	Asp	Thr	Ile	Ile	Phe	Arg	Ser	Thr	Asp	Gly	Gly	Ala	Thr	Trp	Thr	370	375	380	
Arg	Ile	Trp	Asp	Trp	Thr	Ser	Tyr	Pro	Asn	Arg	Ser	Leu	Arg	Tyr	Val	385	390	395	400
Leu	Asp	Ile	Ser	Ala	Glu	Pro	Trp	Leu	Thr	Phe	Gly	Val	Gln	Pro	Asn	405	410	415	
Pro	Pro	Val	Pro	Ser	Pro	Lys	Leu	Gly	Trp	Met	Asp	Glu	Ala	Met	Ala	420	425	430	
Ile	Asp	Pro	Phe	Asn	Ser	Asp	Arg	Met	Leu	Tyr	Gly	Thr	Gly	Ala	Thr	435	440	445	

Leu Tyr Ala Thr Asn Asp Leu Thr Lys Trp Asp Ser Gly Gly Gln Ile
 450 455 460
 His Ile Ala Pro Met Val Lys Gly Leu Glu Glu Thr Ala Val Asn Asp
 465 470 475 480
 Leu Ile Ser Pro Pro Ser Gly Ala Pro Leu Ile Ser Ala Leu Gly Asp
 485 490 495
 Leu Gly Gly Phe Thr His Ala Asp Val Thr Ala Val Pro Ser Thr Ile
 500 505 510
 Phe Thr Ser Pro Val Phe Thr Thr Gly Thr Ser Val Asp Tyr Ala Glu
 515 520 525
 Leu Asn Pro Ser Ile Ile Val Arg Ala Gly Ser Phe Asp Pro Ser Ser
 530 535 540
 Gln Pro Asn Asp Arg His Val Ala Phe Ser Thr Asp Gly Gly Lys Asn
 545 550 555 560
 Trp Phe Gln Gly Ser Glu Pro Gly Gly Val Thr Thr Gly Gly Thr Val
 565 570 575
 Ala Ala Ser Ala Asp Gly Ser Arg Phe Val Trp Ala Pro Gly Asp Pro
 580 585 590
 Gly Gln Pro Val Val Tyr Ala Val Gly Phe Gly Asn Ser Trp Ala Ala
 595 600 605
 Ser Gln Gly Val Pro Ala Asn Ala Gln Ile Arg Ser Asp Arg Val Asn
 610 615 620
 Pro Lys Thr Phe Tyr Ala Leu Ser Asn Gly Thr Phe Tyr Arg Ser Thr
 625 630 635 640
 Asp Gly Gly Val Thr Phe Gln Pro Val Ala Ala Gly Leu Pro Ser Ser
 645 650 655
 Gly Ala Val Gly Val Met Phe His Ala Val Pro Gly Lys Glu Gly Asp
 660 665 670
 Leu Trp Leu Ala Ala Ser Ser Gly Leu Tyr His Ser Thr Asn Gly Gly
 675 680 685
 Ser Ser Trp Ser Ala Ile Thr Gly Val Ser Ser Ala Val Asn Val Gly
 690 695 700
 Phe Gly Lys Ser Ala Pro Gly Ser Ser Tyr Pro Ala Val Phe Val Val
 705 710 715 720
 Gly Thr Ile Gly Gly Val Thr Gly Ala Tyr Arg Ser Asp Asp Cys Gly
 725 730 735
 Thr Thr Trp Val Leu Ile Asn Asp Asp Gln His Gln Tyr Gly Asn Trp
 740 745 750

Gly Gln Ala Ile Thr Gly Asp His Ala Asn Leu Arg Arg Val Tyr Ile
755 760 765

Gly Thr Asn Gly Arg Gly Ile Val Tyr Gly Asp Ile Gly Gly Ala Pro
770 775 780
Cut #3

Ser Gly Ser Pro Ser Pro Ser Val Ser Pro Ser Ala Ser Pro Ser Leu
785 790 795 800

Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro
805 810 815

Ser Ser Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro
820 825 830

Ser Pro Ser Arg Ser Pro Ser Pro Ser Ala Ser Pro Ser Pro Ser Ser
835 840 845

Ser Pro Ser Pro Ser Ser Ser Pro Ser Ser Ser Pro Ser Pro Thr Pro
850 855 860

Ser Ser Ser Pro Val Ser Gly Gly Val Lys Val Gln Tyr Lys Asn Asn
865 870 875 880
Carb BD #4

Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Val Val
885 890 895

Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr
900 905 910

Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp
915 920 925

Trp Ala Ala Ile Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val
930 935 940

Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Xaa
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<210> 2

<211> 2869

<212> DNA

<213> Acidothermus cellulolyticus

<220>

<221> modified_base

<222> (2869)

<223> a, c, t, g, other or unknown

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gcttctcctg cgcacgcggc gacgactcag ccgtacacct ggagcaacgt ggcgatcggg 180
ggcggcggct ttgtcgacgg gatcgtcttc aatgaagggt caccgggaat tctgtacgtg 240
cggacggaca tcggggggat gtatcgatgg gatgccgcca acgggcgggt gatccctctt 300
ctggattggg tgggatggaa caattggggg tacaacggcg tcgtcagcat tgcggcagac 360
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acagattccg gcgcgacctg gtcccagatg acgaactttc cggacgtagg cacgtacatt 660
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gatcccaata atccggtctt ctggagcaga gacggcgggc cgacgtggca ggcggtgccg 840
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<211> 740

<212> PRT

<213> Acidothermus cellulolyticus

<220>

<223> Catalytic domain GH74

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 35 40 45
 Gly Arg Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly
 50 55 60
 Tyr Asn Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys
 65 70 75 80
 Val Trp Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp
 85 90 95
 Gly Ala Ile Leu Arg Ser Ser Asp Gln Gly Ala Thr Trp Gln Ile Thr
 100 105 110
 Pro Leu Pro Phe Lys Leu Gly Gly Asn Met Pro Gly Arg Gly Met Gly
 115 120 125
 Glu Arg Leu Ala Val Asp Pro Asn Asn Asp Asn Ile Leu Tyr Phe Gly
 130 135 140
 Ala Pro Ser Gly Lys Gly Leu Trp Arg Ser Thr Asp Ser Gly Ala Thr
 145 150 155 160
 Trp Ser Gln Met Thr Asn Phe Pro Asp Val Gly Thr Tyr Ile Ala Asn
 165 170 175
 Pro Thr Asp Thr Thr Gly Tyr Gln Ser Asp Ile Gln Gly Val Val Trp
 180 185 190
 Val Ala Phe Asp Lys Ser Ser Ser Ser Leu Gly Gln Ala Ser Lys Thr
 195 200 205
 Ile Phe Val Gly Val Ala Asp Pro Asn Asn Pro Val Phe Trp Ser Arg
 210 215 220
 Asp Gly Gly Ala Thr Trp Gln Ala Val Pro Gly Ala Pro Thr Gly Phe
 225 230 235 240
 Ile Pro His Lys Gly Val Phe Asp Pro Val Asn His Val Leu Tyr Ile
 245 250 255
 Ala Thr Ser Asn Thr Gly Gly Pro Tyr Asp Gly Ser Ser Gly Asp Val
 260 265 270
 Trp Lys Phe Ser Val Thr Ser Gly Thr Trp Thr Arg Ile Ser Pro Val
 275 280 285
 Pro Ser Thr Asp Thr Ala Asn Asp Tyr Phe Gly Tyr Ser Gly Leu Thr
 290 295 300
 Ile Asp Arg Gln His Pro Asn Thr Ile Met Val Ala Thr Gln Ile Ser
 305 310 315 320
 Trp Trp Pro Asp Thr Ile Ile Phe Arg Ser Thr Asp Gly Gly Ala Thr
 325 330 335

Trp Thr Arg Ile Trp Asp Trp Thr Ser Tyr Pro Asn Arg Ser Leu Arg
 340 345 350
 Tyr Val Leu Asp Ile Ser Ala Glu Pro Trp Leu Thr Phe Gly Val Gln
 355 360 365
 Pro Asn Pro Pro Val Pro Ser Pro Lys Leu Gly Trp Met Asp Glu Ala
 370 375 380
 Met Ala Ile Asp Pro Phe Asn Ser Asp Arg Met Leu Tyr Gly Thr Gly
 385 390 395 400
 Ala Thr Leu Tyr Ala Thr Asn Asp Leu Thr Lys Trp Asp Ser Gly Gly
 405 410 415
 Gln Ile His Ile Ala Pro Met Val Lys Gly Leu Glu Glu Thr Ala Val
 420 425 430
 Asn Asp Leu Ile Ser Pro Pro Ser Gly Ala Pro Leu Ile Ser Ala Leu
 435 440 445
 Gly Asp Leu Gly Gly Phe Thr His Ala Asp Val Thr Ala Val Pro Ser
 450 455 460
 Thr Ile Phe Thr Ser Pro Val Phe Thr Thr Gly Thr Ser Val Asp Tyr
 465 470 475 480
 Ala Glu Leu Asn Pro Ser Ile Ile Val Arg Ala Gly Ser Phe Asp Pro
 485 490 495
 Ser Ser Gln Pro Asn Asp Arg His Val Ala Phe Ser Thr Asp Gly Gly
 500 505 510
 Lys Asn Trp Phe Gln Gly Ser Glu Pro Gly Gly Val Thr Thr Gly Gly
 515 520 525
 Thr Val Ala Ala Ser Ala Asp Gly Ser Arg Phe Val Trp Ala Pro Gly
 530 535 540
 Asp Pro Gly Gln Pro Val Val Tyr Ala Val Gly Phe Gly Asn Ser Trp
 545 550 555 560
 Ala Ala Ser Gln Gly Val Pro Ala Asn Ala Gln Ile Arg Ser Asp Arg
 565 570 575
 Val Asn Pro Lys Thr Phe Tyr Ala Leu Ser Asn Gly Thr Phe Tyr Arg
 580 585 590
 Ser Thr Asp Gly Gly Val Thr Phe Gln Pro Val Ala Ala Gly Leu Pro
 595 600 605
 Ser Ser Gly Ala Val Gly Val Met Phe His Ala Val Pro Gly Lys Glu
 610 615 620
 Gly Asp Leu Trp Leu Ala Ala Ser Ser Gly Leu Tyr His Ser Thr Asn
 625 630 635 640

Gly Gly Ser Ser Trp Ser Ala Ile Thr Gly Val Ser Ser Ala Val Asn
 645 650 655
 Val Gly Phe Gly Lys Ser Ala Pro Gly Ser Ser Tyr Pro Ala Val Phe
 660 665 670
 Val Val Gly Thr Ile Gly Gly Val Thr Gly Ala Tyr Arg Ser Asp Asp
 675 680 685
 Cys Gly Thr Thr Trp Val Leu Ile Asn Asp Asp Gln His Gln Tyr Gly
 690 695 700
 Asn Trp Gly Gln Ala Ile Thr Gly Asp His Ala Asn Leu Arg Arg Val
 705 710 715 720
 Tyr Ile Gly Thr Asn Gly Arg Gly Ile Val Tyr Gly Asp Ile Gly Gly
 725 730 735
 Ala Pro Ser Gly
 740

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 <212> PRT
 <213> Acidothermus cellulolyticus

<220>
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 <222> (89)
 <223> Any amino acid

<220>
 <223> Carbohydrate binding domain

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 Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
 35 40 45
 Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
 50 55 60
 Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
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 Pro Thr Ala Asp Thr Tyr Leu Gln Xaa only Δ w/ #5
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<212> PRT

<213> Acidothermus cellulolyticus

<220>

<223> Carbohydrate binding domain

<400> 5

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20 25 30

Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
35 40 45

Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
50 55 60

Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
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Pro Thr Ala Asp Thr Tyr Leu Gln
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<211> 740

<212> PRT

<213> Acidothermus cellulolyticus

<400> 6

Ala Thr Thr Gln Pro Tyr Thr Trp Ser Asn Val Ala Ile Gly Gly Gly
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20 25 30

Tyr Val Arg Thr Asp Ile Gly Gly Met Tyr Arg Trp Asp Ala Ala Asn
35 40 45

Gly Arg Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly
50 55 60

Tyr Asn Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys
65 70 75 80

Val Trp Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp
85 90 95

Gly Ala Ile Leu Arg Ser Ser Asp Gln Gly Ala Thr Trp Gln Ile Thr
100 105 110

Pro Leu Pro Phe Lys Leu Gly Gly Asn Met Pro Gly Arg Gly Met Gly
115 120 125

Glu	Arg	Leu	Ala	Val	Asp	Pro	Asn	Asn	Asp	Asn	Ile	Leu	Tyr	Phe	Gly	130	135	140
Ala	Pro	Ser	Gly	Lys	Gly	Leu	Trp	Arg	Ser	Thr	Asp	Ser	Gly	Ala	Thr	145	150	155
Trp	Ser	Gln	Met	Thr	Asn	Phe	Pro	Asp	Val	Gly	Thr	Tyr	Ile	Ala	Asn	165	170	175
Pro	Thr	Asp	Thr	Thr	Gly	Tyr	Gln	Ser	Asp	Ile	Gln	Gly	Val	Val	Trp	180	185	190
Val	Ala	Phe	Asp	Lys	Ser	Ser	Ser	Ser	Leu	Gly	Gln	Ala	Ser	Lys	Thr	195	200	205
Ile	Phe	Val	Gly	Val	Ala	Asp	Pro	Asn	Asn	Pro	Val	Phe	Trp	Ser	Arg	210	215	220
Asp	Gly	Gly	Ala	Thr	Trp	Gln	Ala	Val	Pro	Gly	Ala	Pro	Thr	Gly	Phe	225	230	235
Ile	Pro	His	Lys	Gly	Val	Phe	Asp	Pro	Val	Asn	His	Val	Leu	Tyr	Ile	245	250	255
Ala	Thr	Ser	Asn	Thr	Gly	Gly	Pro	Tyr	Asp	Gly	Ser	Ser	Gly	Asp	Val	260	265	270
Trp	Lys	Phe	Ser	Val	Thr	Ser	Gly	Thr	Trp	Thr	Arg	Ile	Ser	Pro	Val	275	280	285
Pro	Ser	Thr	Asp	Thr	Ala	Asn	Asp	Tyr	Phe	Gly	Tyr	Ser	Gly	Leu	Thr	290	295	300
Ile	Asp	Arg	Gln	His	Pro	Asn	Thr	Ile	Met	Val	Ala	Thr	Gln	Ile	Ser	305	310	315
Trp	Trp	Pro	Asp	Thr	Ile	Ile	Phe	Arg	Ser	Thr	Asp	Gly	Gly	Ala	Thr	325	330	335
Trp	Thr	Arg	Ile	Trp	Asp	Trp	Thr	Ser	Tyr	Pro	Asn	Arg	Ser	Leu	Arg	340	345	350
Tyr	Val	Leu	Asp	Ile	Ser	Ala	Glu	Pro	Trp	Leu	Thr	Phe	Gly	Val	Gln	355	360	365
Pro	Asn	Pro	Pro	Val	Pro	Ser	Pro	Lys	Leu	Gly	Trp	Met	Asp	Glu	Ala	370	375	380
Met	Ala	Ile	Asp	Pro	Phe	Asn	Ser	Asp	Arg	Met	Leu	Tyr	Gly	Thr	Gly	385	390	395
Ala	Thr	Leu	Tyr	Ala	Thr	Asn	Asp	Leu	Thr	Lys	Trp	Asp	Ser	Gly	Gly	405	410	415
Gln	Ile	His	Ile	Ala	Pro	Met	Val	Lys	Gly	Leu	Glu	Glu	Thr	Ala	Val	420	425	430

Asn	Asp	Leu	Ile	Ser	Pro	Pro	Ser	Gly	Ala	Pro	Leu	Ile	Ser	Ala	Leu	435	440	445	
Gly	Asp	Leu	Gly	Gly	Phe	Thr	His	Ala	Asp	Val	Thr	Ala	Val	Pro	Ser	450	455	460	
Thr	Ile	Phe	Thr	Ser	Pro	Val	Phe	Thr	Thr	Gly	Thr	Ser	Val	Asp	Tyr	465	470	475	480
Ala	Glu	Leu	Asn	Pro	Ser	Ile	Ile	Val	Arg	Ala	Gly	Ser	Phe	Asp	Pro	485	490	495	
Ser	Ser	Gln	Pro	Asn	Asp	Arg	His	Val	Ala	Phe	Ser	Thr	Asp	Gly	Gly	500	505	510	
Lys	Asn	Trp	Phe	Gln	Gly	Ser	Glu	Pro	Gly	Gly	Val	Thr	Thr	Gly	Gly	515	520	525	
Thr	Val	Ala	Ala	Ser	Ala	Asp	Gly	Ser	Arg	Phe	Val	Trp	Ala	Pro	Gly	530	535	540	
Asp	Pro	Gly	Gln	Pro	Val	Val	Tyr	Ala	Val	Gly	Phe	Gly	Asn	Ser	Trp	545	550	555	560
Ala	Ala	Ser	Gln	Gly	Val	Pro	Ala	Asn	Ala	Gln	Ile	Arg	Ser	Asp	Arg	565	570	575	
Val	Asn	Pro	Lys	Thr	Phe	Tyr	Ala	Leu	Ser	Asn	Gly	Thr	Phe	Tyr	Arg	580	585	590	
Ser	Thr	Asp	Gly	Gly	Val	Thr	Phe	Gln	Pro	Val	Ala	Ala	Gly	Leu	Pro	595	600	605	
Ser	Ser	Gly	Ala	Val	Gly	Val	Met	Phe	His	Ala	Val	Pro	Gly	Lys	Glu	610	615	620	
Gly	Asp	Leu	Trp	Leu	Ala	Ala	Ser	Ser	Gly	Leu	Tyr	His	Ser	Thr	Asn	625	630	635	640
Gly	Gly	Ser	Ser	Trp	Ser	Ala	Ile	Thr	Gly	Val	Ser	Ser	Ala	Val	Asn	645	650	655	
Val	Gly	Phe	Gly	Lys	Ser	Ala	Pro	Gly	Ser	Ser	Tyr	Pro	Ala	Val	Phe	660	665	670	
Val	Val	Gly	Thr	Ile	Gly	Gly	Val	Thr	Gly	Ala	Tyr	Arg	Ser	Asp	Asp	675	680	685	
Cys	Gly	Thr	Thr	Trp	Val	Leu	Ile	Asn	Asp	Asp	Gln	His	Gln	Tyr	Gly	690	695	700	
Asn	Trp	Gly	Gln	Ala	Ile	Thr	Gly	Asp	His	Ala	Asn	Leu	Arg	Arg	Val	705	710	715	720
Tyr	Ile	Gly	Thr	Asn	Gly	Arg	Gly	Ile	Val	Tyr	Gly	Asp	Ile	Gly	Gly	725	730	735	

Ala Pro Ser Gly
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Ala Tyr Ala Arg Thr Asp Ile Gly Gly Ala Tyr Arg Leu Asn Ser Asp
35 40 45

Asp Thr Trp Thr Pro Leu Met Asp Trp Val Gly Asn Asp Thr Trp His
50 55 60

Asp Trp Gly Ile Asp Ala Leu Ala Thr Asp Pro Val Asp Thr Asp Arg
65 70 75 80

Val Tyr Val Ala Val Gly Met Tyr Thr Asn Glu Trp Asp Pro Asn Val
85 90 95

Gly Ser Ile Leu Arg Ser Thr Asp Gln Gly Asp Thr Trp Thr Glu Thr
100 105 110

Lys Leu Pro Phe Lys Val Gly Gly Asn Met Pro Gly Arg Gly Met Gly
115 120 125

Glu Arg Leu Ala Val Asp Pro Asn Lys Asn Ser Ile Leu Tyr Phe Gly
130 135 140

Ala Arg Ser Gly His Gly Leu Trp Lys Ser Thr Asp Tyr Gly Ala Thr
145 150 155 160

Trp Ser Asn Val Thr Ser Phe Thr Trp Thr Gly Thr Tyr Phe Gln Asp
165 170 175

Ser Ser Ser Thr Tyr Thr Ser Asp Pro Val Gly Ile Ala Trp Val Thr
180 185 190

Phe Asp Ser Thr Ser Gly Ser Ser Gly Ser Ala Thr Pro Arg Ile Phe
195 200 205

Val Gly Val Ala Asp Ala Gly Lys Ser Val Phe Lys Ser Glu Asp Ala
210 215 220

Gly Ala Thr Trp Ala Trp Val Ser Gly Glu Pro Gln Tyr Gly Phe Leu
225 230 235 240

Pro His Lys Gly Val Leu Ser Pro Glu Glu Lys Thr Leu Tyr Ile Ser
245 250 255

Tyr Ala Asn Gly Ala Gly Pro Tyr Asp Gly Thr Asn Gly Thr Val His
 260 265 270
 Lys Tyr Asn Ile Thr Ser Gly Val Trp Thr Asp Ile Ser Pro Thr Ser
 275 280 285
 Leu Ala Ser Thr Tyr Tyr Gly Tyr Gly Gly Leu Ser Val Asp Leu Gln
 290 295 300
 Val Pro Gly Thr Leu Met Val Ala Ala Leu Asn Cys Trp Trp Pro Asp
 305 310 315 320
 Glu Leu Ile Phe Arg Ser Thr Asp Ser Gly Ala Thr Trp Ser Pro Ile
 325 330 335
 Trp Glu Trp Asn Gly Tyr Pro Ser Ile Asn Tyr Tyr Tyr Ser Tyr Asp
 340 345 350
 Ile Ser Asn Ala Pro Trp Ile Gln Asp Thr Thr Ser Thr Asp Gln Phe
 355 360 365
 Pro Val Arg Val Gly Trp Met Val Glu Ala Leu Ala Ile Asp Pro Phe
 370 375 380
 Asp Ser Asn His Trp Leu Tyr Gly Thr Gly Leu Thr Val Tyr Gly Gly
 385 390 395 400
 His Asp Leu Thr Asn Trp Asp Ser Lys His Asn Val Thr Val Lys Ser
 405 410 415
 Leu Ala Val Gly Ile Glu Glu Met Ala Val Leu Gly Leu Ile Thr Pro
 420 425 430
 Pro Gly Gly Pro Ala Leu Leu Ser Ala Val Gly Asp Asp Gly Gly Phe
 435 440 445
 Tyr His Ser Asp Leu Asp Ala Ala Pro Asn Gln Ala Tyr His Thr Pro
 450 455 460
 Thr Tyr Gly Thr Thr Asn Gly Ile Asp Tyr Ala Gly Asn Lys Pro Ser
 465 470 475 480
 Asn Ile Val Arg Ser Gly Ala Ser Asp Asp Tyr Pro Thr Leu Ala Leu
 485 490 495
 Ser Ser Asn Phe Gly Ser Thr Trp Tyr Ala Asp Tyr Ala Ala Ser Thr
 500 505 510
 Ser Thr Gly Thr Gly Ala Val Ala Leu Ser Ala Asp Gly Asp Thr Val
 515 520 525
 Leu Leu Met Ser Ser Thr Ser Gly Ala Leu Val Ser Lys Ser Gln Gly
 530 535 540
 Thr Leu Thr Ala Val Ser Ser Leu Pro Ser Gly Ala Val Ile Ala Ser
 545 550 555 560

Asp Lys Ser Asp Asn Thr Val Phe Tyr Gly Gly Ser Ala Gly Ala Ile
 565 570 575
 Tyr Val Ser Lys Asn Thr Ala Thr Ser Phe Thr Lys Thr Val Ser Leu
 580 585 590
 Gly Ser Ser Thr Thr Val Asn Ala Ile Arg Ala His Pro Ser Ile Ala
 595 600 605
 Gly Asp Val Trp Ala Ser Thr Asp Lys Gly Leu Trp His Ser Thr Asp
 610 615 620
 Tyr Gly Ser Thr Phe Thr Gln Ile Gly Ser Gly Val Thr Ala Gly Trp
 625 630 635 640
 Ser Phe Gly Phe Gly Lys Ala Ser Ser Thr Gly Ser Tyr Val Val Ile
 645 650 655
 Tyr Gly Phe Phe Thr Ile Asp Gly Ala Ala Gly Leu Phe Lys Ser Glu
 660 665 670
 Asp Ala Gly Thr Asn Trp Gln Val Ile Ser Asp Ala Ser His Gly Phe
 675 680 685
 Gly Ser Gly Ser Ala Asn Val Val Asn Gly Asp Leu Gln Thr Tyr Gly
 690 695 700
 Arg Val Phe Arg Gly His Glu Arg Pro Gly His Leu Leu Arg Gln Ser
 705 710 715 720
 Gln Arg Glu Pro Ala Gly
 725